WEST Search History

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DATE: Thursday, September 27, 2007

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT; PLUR=YES; OP=OR	
☐	L11	l9 and L10	13
☐	L10	long with sage	88
☐	L9	(organism or organism$ or species or taxonom$) same (complex$ or divers$)	61614
☐	L8	l6 and L7	8
☐	L7	(organism or organism$ or species) same (complex$ or divers$)	61170
☐	L6	long with SAGE and genom$ with (tag or tag$)	14
☐	L5	(organism or organism$) with (complex$ or divers$) and long with SAGE and genom$ with (tag or tag$)	8
☐	L4	(organism or organism$) with (complex$ or divers$) and l3	2
☐	L3	long with SAGE same genom$ with (tag or tag$)	6
☐	L2	long with SAGE same signature with (tag or tag$)	0
☐	L1	long with SAGE same genom$ with signature with (tag or tag$)	0

END OF SEARCH HISTORY

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    NEWS 1   Web Page for STN Seminar Schedule - N. America
    NEWS 2   JUL 02   LMEDLINE coverage updated
    NEWS 3   JUL 02   SCISEARCH enhanced with complete author names
    NEWS 4   JUL 02   CHEMCATS accession numbers revised
    NEWS 5   JUL 02   CA/CAplus enhanced with utility model patents from China
    NEWS 6   JUL 16   CAplus enhanced with French and German abstracts
    NEWS 7   JUL 18   CA/CAplus patent coverage enhanced
    NEWS 8   JUL 26   USPATFULL/USPAT2 enhanced with IPC reclassification
    NEWS 9   JUL 30   USGENE now available on STN
    NEWS 10   AUG 06. CAS REGISTRY enhanced with new experimental property tags
    NEWS 11   AUG 06   BEILSTEIN updated with new compounds
    NEWS 12   AUG 06   FSTA enhanced with new thesaurus edition
    NEWS 13   AUG 13   CA/CAplus enhanced with additional kind codes for granted
                       patents
    NEWS 14   AUG 20   CA/CAplus enhanced with CAS indexing in pre-1907 records
    NEWS 15   AUG 27   Full-text patent databases enhanced with predefined
                       patent family display formats from INPADOCDB
    NEWS 16   AUG 27   USPATOLD now available on STN
    NEWS 17   AUG 28   CAS REGISTRY enhanced with additional experimental
                       spectral property data
    NEWS 18   SEP 07   STN AnaVist, Version 2.0, now available with Derwent
                       World Patents Index
    NEWS 19   SEP 13   FORIS renamed to SOFIS
    NEWS 20   SEP 13   INPADOCDB enhanced with monthly SDI frequency
    NEWS 21   SEP 17   CA/CAplus enhanced with printed CA page images from
                       1967-1998
    NEWS 22   SEP 17   CAplus coverage extended to include traditional medicine
                       patents
    NEWS 23   SEP 24   EMBASE, EMBAL, and LEMBASE reloaded with enhancements

    NEWS EXPRESS   19 SEPTEMBER 2007: CURRENT WINDOWS VERSION IS V8.2,
                   CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
                   AND CURRENT DISCOVER FILE IS DATED 19 SEPTEMBER 2007.

    NEWS HOURS   STN Operating Hours Plus Help Desk Availability
    NEWS LOGIN   Welcome Banner and News Items
    NEWS IPC8   For general information regarding STN implementation of IPC 8

Enter NEWS followed by the item number or name to see news on that
specific topic.

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* * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 09:06:02 ON 27 SEP 2007

=> fil medline biosis caplus scisearch embase wpids
COST IN U.S. DOLLARS                              SINCE FILE    TOTAL
                                                   ENTRY       SESSION
FULL ESTIMATED COST                                0.21         0.21


FILE 'MEDLINE' ENTERED AT 09:06:41 ON 27 SEP 2007

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=> long (s) sage
L1          354 LONG (S) SAGE

=> (organism or organism? or species or taxonom?) (s) (complex? or divers?)
   2 FILES SEARCHED...
L2       237306 (ORGANISM OR ORGANISM? OR SPECIES OR TAXONOM?) (S) (COMPLEX? OR
                DIVERS?)

=> l1 and l2
L3            1 L1 AND L2

=> d ibib abs l3

L3    ANSWER 1 OF 1   BIOSIS   COPYRIGHT (c) 2007 The Thomson Corporation   on STN
ACCESSION NUMBER:     2001:519183   BIOSIS
DOCUMENT NUMBER:      PREV200100519183
TITLE:                High-throughput DNA sequencing and analysis of Micro-SAGE
                      libraries using MegaBACE 1000 to study hippocampal
                      transcriptome.
AUTHOR(S):            Fan, Qing-Qing [Reprint author]; Jones, Gregg S.; Edwards,
                      John R.; Richlin-Zack, Kate; Kandel, Eric R. [Reprint
                      author]; Ju, Jingyue
CORPORATE SOURCE:     Center of Neurobiology, College of Physicians and Surgeons,
                      Howard Hughes Medical Institute, Columbia University, New
                      York, NY, USA
SOURCE:               International Genome Sequencing and Analysis Conference,
                      (2000) Vol. 12, pp. 69. print.
                      Meeting Info.: 12th International Genome Sequencing and
                      Analysis Conference. Miami Beach, Florida, USA. September
                      12-15, 2000.
DOCUMENT TYPE:        Conference; (Meeting)
                      Conference; Abstract; (Meeting Abstract)
                      Conference; (Meeting Poster)
LANGUAGE:             English
ENTRY DATE:           Entered STN: 7 Nov 2001
```

AB   Transcriptomes, the temporal and spatial expression patterns of genes in
     an organism, represent an important level of dynamic functional
     biological complexity. Studies of transcriptomes of different
     conditions will provide insight into the molecular basis of biological
     processes. High-throughput methods, such as Microarray and Serial
     Analysis of Gene Expression (SAGE) techniques, are highly effective in
     capturing snapshots of transcriptomes. In the study of genes related to
     long-term memory using Micro-SAGE, a modified
     SAGE method requiring much less starting materials, we have
     sequenced over 40,000 transcript tags from a mouse hippocampal
     SAGE library using MegaBACE 1000 capillary array DNA sequencers
     with DYEnamic ET Terminators. We incorporated a modified PCR protocol to
     amplify SAGE concatenants for high-throughput sequencing. We have also
     developed a post-sequencing data analysis protocol that includes Phred
     basecalling and Phrap assembly software to assign confidence scores and
     align sequences from both the 5' and 3' directions. We then used CONSED
     to perform the final manual editing of low quality regions in the
     electropherograms and thereby attained a high fidelity consensus sequence.
     The quality of our automated data analysis was evaluated against the
     manual analysis of more than 20,000 tags, and the results are comparable.
     Thus, we have developed a high-throughput DNA sequencing method for the
     analysis of SAGE libraries using MegaBACE 1000.

=> d his

     (FILE 'HOME' ENTERED AT 09:06:02 ON 27 SEP 2007)

     FILE 'MEDLINE, BIOSIS, CAPLUS, SCISEARCH, EMBASE, WPIDS' ENTERED AT
     09:06:41 ON 27 SEP 2007
L1   354 LONG (S) SAGE
L2   237306 (ORGANISM OR ORGANISM? OR SPECIES OR TAXONOM?) (S) (COMPLEX? OR
L3   1 L1 AND L2

=> logoff hold
COST IN U.S. DOLLARS   SINCE FILE   TOTAL
                                                 ENTRY   SESSION
FULL ESTIMATED COST   33.26   33.47

 SESSION WILL BE HELD FOR 120 MINUTES
STN INTERNATIONAL SESSION SUSPENDED AT 09:12:22 ON 27 SEP 2007